

Figure 1A

1	CAAGCACTGTGCTAAAGTGT	TTTCATATGTCATGAAAAGTGTGCCAGAAAATTATGGT	60
61	TTGAACATGGCAGTTCTCCTACCGTCAGCTATATCCACAAAGCATCACATGAAGTGG	A	120
121	GATCTGGCAGCTCTGTGTTACGTCAAGTTCCACAATGAAACCTGACAATAATGGTAA	A	180
181	AAACCAATACGGACATCTGAGTA	ACTGGGATTGGCCTGCCTGCATGTGAGCTTGATG	240
241	GAAGATTGGATATAGACGAGTTGATTATTTATGAAGTAGCAGCTCACTACCATCCAC	M A L S G N C S R	300
301	CATCCAGGGTTAAACTACTTTTCAGCATCACTTCACCTGACTCTTACATTTTG	A	360
361	ATTTCTGGGGAAAAACTGGATAAGAGGAGGTCA	TTTTTAATAAAGTTAGCATCCT	420
421	TTTCCCTTCTTACAAGTTGATCCAAGGATAAGGCTGTGACTCCATTGGATTGCACCTT	A	480
481	TAAATCAAATAGCAGCAGCAGAAGAAGGGACAATGGCTCTGAGTGGAAACTGTAGTCG	M A L S G N C S R	540
1	Y Y P R E Q G S A V P N S F P E V V E L	A	9
541	TTATTATCCTCGAGAACAAAGGTCCGAGTTCCCAACTCCTCCCTGAGGTGGTAGAGCT	M A L S G N C S R	600
10	Y Y P R E Q G S A V P N S F P E V V E L	A	29
601	GAATGTCGGGGGTCAAGTTTATTTACTCGCATTCCACATTGATAAGCATCCCTCATTC	N V G G Q V Y F T R H S T L I S I P H S	660
30	L W K M F S P K R D T A N D L A K D S	A	49
661	CCTCTGTGAAAATGTTTCCCAAGAGAGACACGGCTAATGATCTAGCCAAGGACTC	M A L S G N C S R	720
50	L W K M F S P K R D T A N D L A K D S	A	69
721	CAAGGGAAAGGTTTTCATTGACAGAGATGGATTCTTGTCCGTTATATTCTGGACTATCT	K G R F F I D R D G F L F R Y I L D Y L	780
70	K G R F F I D R D G F L F R Y I L D Y L	A	89
781	CAGGGACAGGCAGGTGGCTCTGCCGTGATCACTTCCAGAAAAAGGAAGACTGAAAAGGGA	R D R Q V V L P D H F P E K G R L K R E	840
90	R D R Q V V L P D H F P E K G R L K R E	A	109
841	AGCTGAATACCTCCACCTCCAGACTTGGCTCAAACCTCTGACCCCCGATGAAATCAAGCA	A E Y F Q L P D L V K L L T P D E I K Q	900
110	A E Y F Q L P D L V K L L T P D E I K Q	A	129
901	AAGCCCAGATGAATTCTGCCACAGTCAGTTGAGATGCCCTCCAAAGGAAGCGACACAAG	S P D E F C H S D F E D A S Q G S D T R	960
130	S P D E F C H S D F E D A S Q G S D T R	A	149
961	AATCTGCCCTTCCCTGCCGACCGCAAGTGGGTTTCATTACTGTGGG	I C P P S S L L P A D R K W G F I T V G	1020
150	I C P P S S L L P A D R K W G F I T V G	A	169

Figure 1B

1021	TTACAGAGGATCCTGCACCCTGGGAGAGAGGGACAGGCCAGATGCCAAGTTCGGAGAGT	1080
170	Y R G S C T L G R E G Q A D A K F R R V	189
1081	TCCCCGGATTTGGTTGTGGAAAGGATTCCCTGGCAAAAAGAAGTCTTGGAGAAACTTT	1140
190	P R I L V C G R I S L A K E V F G E T L	209
1141	GAATGAAAGCAGAGACCCCTGATCGAGCCCCAGAAAGATAACACCTCCAGATTCTCAA	1200
210	N E S R D P D R A P . E R Y T S R F Y L K	229
1201	ATTCAAGCACCTGGAAAGGGCTTTGATATGTTGTCAGAGTGTGGATTCCACATGGGCC	1260
230	F K H L E R A F D M L S E C G F H M V A	249
1261	CTGTAACTCATCGGTGACAGCATCTTCATCAACCAATATAACAGATGACAAGATCTGGTC	1320
250	C N S S V T A S F I N Q Y T D D K I W S	269
1321	AAGCTACACTGAATATGTCCTCTACCGTGAGCCCTCCAGATGGTCACCCCTCACACTGCGA	1380
270	S Y T E Y V F Y R E P S R W S P S H C D	289
1381	TTGCTGCTGCAAGAACATGGAAAGGTGACAAAGAAGGGGAGAGCGGCACGTCTTGCAATGA	1440
290	C C C K N G K G D K E G E S G T S C N D	309
1441	CCTCTCCACATCTAGCTGGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCAT	1500
310	L S T S S C D S Q S E A S S P Q E T V I	329
1501	CTGTTGGTCCCGTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCCATAAGAACAGG	1560
330	C G P V T R Q T N I Q T L D R P I K K G	349
1561	CCCTGTCCAGCTGATCCAACAGTCAGAGATGCCGGCGAAAAGCGACTTACTCCGGATTC	1620
350	P V Q L I Q Q S E M R R K S D L L R I L	369
1621	GACTTCAGGCTCCAGGGAAATCGAACATGAGCAGCAAAAAAAAGCTGTTAAAGAAAAGCT	1680
370	T S G S R E S N M S S K K K A V K E K L	389
1681	CTCAATTGAGGAGGAGCTGGAGAAATGATCCAGGATTCTCTAAAAAAATCCAGA	1740
390	S I E E E L E K C I Q D F L K K K I P D	409
1741	TCGGTTTCCTGAGAGAAAAACATCCTGGCAATCTGAACTTTAAGGAAGTATCATCTATA	1800
410	R F P E R K H P W Q S E L L R K Y H L	428
1801	AGGGAGGGCTGGGGCGGGAAAAAAAGAGTCATTTGAAATTACCTCATAA	1860
1861	AAGGAATTCATATTTAAAGGAAAAAAATCAACTAATGATGCACATTCTTAGAACACA	1920
1921	ATAGTCCATTGATATACTACTGCCTACTTACCTAGTTACCTAACATGTAATCCACA	1980

**Figure 1C**

1981	GGGTAGATTTCTTCTAGATGTGGAAGTACAAGAAAATCTTTTAGTTATTGTTGTT	2040
2041	TACTCGTCCCAGTGCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAGTAGC	2100
2101	TGAGAGGCCCTGGGAGTCATTATCCCCAACTGGGTTTTCTCTCATCCTCTACCTCC	2160
2161	CTCCTTGAAATGAGGGTATGGTAGAAAAAGATCTGGCCAATGGCATAAGTTGGAATT	2220
2221	TTAATTTGGTTTCTTTGTTATGGGTTGGGGGAATGGCAGATTATATGACTT	2280
2281	TTCACCTAAATCTATATGTGCCAGTTATATTGACTCCGTATGCATGAGTATTGTGCAA	2340
2341	CACAAGCACAACAACTAAGTATGTATACACATGACGCACACGATGCCAGGCCTAGACCTC	2400
2401	CCAAGGGCTGTGCTCTGCTCCCAGCAGCCCTCTTCTAGAATATTCAGATGGATGAGCT	2460
2461	TCTGACTCTTCTAAATCTTTGGGAAGATTCCAGCCTTCTTCACAACACTTTC	2520
2521	TAACATCAAATGACTCTCATCAACAAATTGTATTCTTATTGTGAAATTAATACCCT	2580
2581	CAGGCTCCATTACTGCTTGCTCTTGCTGCTTAAGAGAGGATGGAGAGCTGGT	2640
2641	CAAACATTCTTGTTAAAAAAATCAAACATTCAATCCACAAAATTCTGCTAAATG	2700
2701	ACTCCACACTCAGCCTCTCACCCCTGAACTGAATTATCACCCCTTCTCCATGTTCA	2760
2761	GAGTTCTTACTGCCAACAGTTAATGGTGTGCCCTTCCACATAATCCACATTAAGTTCT	2820
2821	GTGTTCTGTGTTGTGGAACTAAGGAAACACACAGTACTGAAATAAGGTCGGCC	2880
2881	TTTTGTTTTAGAGAAAGTTGTATTCCACACACACCTAATAATTCTTATAAAAAT	2940
2941	TTTAAACTACAAAGCTACATTTTACTGCTGTAGCCGTTTGTGCTTGGGATT	3000
3001	CGGGCTTGGCTGTGCCCATGCTAGGATTAGCTGTGTCATTATGATGTCATGAA	3060
3061	ACCCACAAAGTAACGAAAGCTCCAGAGTTAAGGTTCAAGATTCTAAATGAAACTATCT	3120
3121	TTTTCAATTACATCCTGACTTGTATAGACACAGCCAAAAGAAAATGTTAATGCCATCC	3180

**Figure 1D**

3181	GTCCATGTAACCTCTGTATTCTACTAAGGTACCAATAGCTCTTCATAGACTTGTGCTACA	3240
3241	AGAAGGTTAAAAGACCAGTTTATTTCAGCATTCCTCATGCATTCAGTGGTAACCAAA	3300
3301	AAATAATTGTCATTAAATAGTTGTGCCAAGCACTCCTAATTGTTTATTGCGTGTG	3360
3361	TGTGCATGTGTATGTATCACAGGTAAATAAGGCAATTGGATGATTTAAAAAAAAAA	3420
3421	AAA 3468	

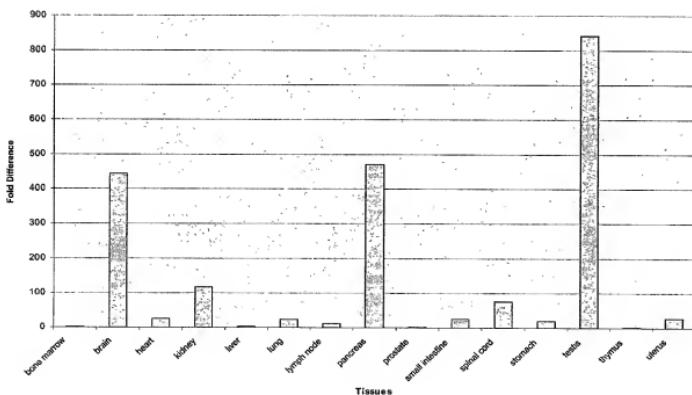
Figure 2A

K+betaM2	(1)	-----MALSGNCNSRYYPREQGSAPNPEPVELNVGGQVTPRREST	50
AAF558201	(1)	-----MPTEELNLNVGGVSTTTLTLPYLO	
CAA20329_1	(1)	-----MTSVEDVITLNVGQVTTTTSLSK	
Y34129	(1)	-----MDNGDWGYMTDPVTLNVGGHLYTTSLSK	
Y34125	(1)	-----MSRPLITRSPASPLXNQGIPTPAQLTKSNAVPVHVGGEHYISSLATL	
	51		100
K+betaM2	(46)	IPHSLLWKMFSP--KRDTANDLAADSKGRFEEIDRDGFIFRVLIDMLRQD	
AAF558201	(24)	DKSLLAEFFG--EGRDSLAKADSKGRVETIDRDGVLFRLVYIDLEDRDKA	
CAA20329_1	(27)	ETTULLENASGSLSEDAQANVYLPGTLEIDRDGPLFVWHLHFLRTD	
Y34129	(33)	YPDSSLQAFGGA---D--FPIDARPQGNYEIDRDGPLFERYILNPLRTE	
Y34125	(51)	YPERSIAGRFDFG---T-EPIVIMLSLKHYEIDRDQGFERVILNPLRTE	
	101		150
K+betaM2	(94)	MVPLPHFPEKGRLKGEAFYFOLPDLWKLILTPDEIKQSPDEFCHSDFEDAS	
AAF558201	(69)	LHLPLQGPFERQRQLRQEAEHFKLTAEMECRSEEDAR	
CAA20329_1	(77)	LSLIPQKFREVAPEKKAADYVSLERFSTLLSNASSIS-PRPR-	
Y34129	(77)	LTLPLDFKEFDLPLRDAFLQLEPFCQLNDPFLPLY	
Y34125	(96)	LLPQKEDYTLTLYEAKVTFQLOPMILEMERWKODR-	
	151		200
K+betaM2	(144)	QGSQTRICPPSSLLPADRKWGFITVYGRGCCTLGREGOADDKFRVPPRL	
AAF558201	(105)	-----PP--GCITVYGRGCFQFCGFLGLADYKFRFESRL	
CAA20329_1	(117)	-----TANGYNTITSAETGGYTTLGRYRHFPAFCRGQADYKFRFARL	
Y34129	(113)	-----PMDFEEVWELSTRKLSKSYSPVAVVITDITITK	
Y34125	(132)	-----EIDGRFSRCPCECLVVRVAPDLGERITLGCBSKSLIEVE	
	201		250
K+betaM2	(194)	VCGRISLKEVPTETLNESRDPDR-APEVRYISRFYLYFKFLLERAFDMLSE	
AAF558201	(137)	VCGRAQCREVFGDTLNESRDPDHGGTTRYTSRFLKHCIEQAFNLHD	
CAA20329_1	(162)	VCGRATLCEVFADTLNESRDPGG--PDCE	
Y34129	(149)	VHLLLEGISNYPTKNNNNIMMDRD-CQVFSTFGPCDYHQEVLSLVHLM	
Y34125	(169)	PEIGDVMCNCSVNAQWNHESTAVIR-----FPLNGYCHLNSVQLERLQQ	
	251		300
K+betaM2	(243)	CGHHIVRCNSSVTASFIN----QYTDDKIWSSTYEVFYVRFPSRWSPSH	
AAF558201	(187)	HGSQHAGSCGSGTAGSAAEPKPGVDTEENRNWHYNEVFIR-----	
CAA20329_1	(191)	-----	
Y34129	(196)	EYTKQGETIIRNTRVHHMSERANENTVHNWTFCRLARKTDD-----	
Y34125	(213)	RGEITVGSCGGYDSSQFSEYVLRRELRTPRVFSVIRIKQ-----PL	
	301		350
K+betaM2	(288)	CDCCKCKNGKDKEGESGTSCNDLSTSSCDSQEASSPQETVICGPVTQQT	
AAF558201	(229)	-----	
CAA20329_1	(191)	-----	
Y34129	(238)	-----	
Y34125	(257)	-----	
	351		400
K+betaM2	(338)	NIQTLDRPIKKGPVQLIQQSEMRRKS DLLRILTSGSRESNMSSKKAVKE	
AAF558201	(229)	-----	
CAA20329_1	(191)	-----	
Y34129	(238)	-----	
Y34125	(257)	-----	

Figure 2B

	401	441
K+betaM2	(388) KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL	
AAF558201	(229) -----	
CAA20329.1	(191) -----	
Y34129	(238) -----	
Y34125	(257) -----	
Consensus	(401)	

Figure 3



**Figure 4.**

Protein	Genbank ID	Identities	Similarities
Human potassium channel K+Hnov28	gi Y34129	31%	41%
Drosophila CG10830 protein	gi AAF55820.1	52%	66%
Caenorhabditis K+ channel tetramerisation domain	gi CAA20329.1	42%	51%
Human potassium channel K+Hnov27	gi Y34125	32%	41%

**Figure 5**

